

SEQUENCE LISTING

<110> Tang et al.

<120> METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

<130> 28110/37260

<140>

<141> 2001-06-28

<150> To be assigned

<151> 2001-04-05

<150> 60/266,614

<151> 2001-02-05

<150> 60/215,733

<151> 2000-06-28

<150> 09/757,562

<151> 2001-01-09

<150> 09/543,774

<151> 2000-04-05

<160> 48

<170> PatentIn version 3.0

<210> 1

<211> 301

<212> DNA

<213> Homo sapiens

<400> 1

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gtaaagaagc aatacctgac agcaaaagtc tggaatccag caaagaaatc ccagagcaac 120

gagaaaacaa acagcagcag aagaagcga aagtccaaga taaacagaaa tcggtatcag 180

tcagcactgt acactagagg gttccatgag attattgtag actcatgatg ctgctatctc 240

aaccagatgc ccaggacagg tgctctagcc attaggacca caaatggaca tgtcagttat 300

t 301

<210> 2

<211> 392

<212> DNA

<213> Homo sapiens

<400> 2

09894912.062801

sub
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 tttcaacaaa gatttctgca caaaatgtaa aagtggattt tacttacacc ttggaaagtg 120
 ccttgacaat tgcccagaag ggttggaaagc caacaaccat actatggagt gtgtcagtat 180
 tgtgcactgt gaggtcagtg aatggaatcc ttggagtcca tgcacgaaga agggaaaaac 240
 atgtggcttc aaaagaggga ctgaaacacg ggtccgagaa ataatacagc atccttcagc 300
 aaagggtaac ctatgtcccc caacaaatga gacaagaaag tgtacagtgc aaaggaagaa 360
 gtgtcagaag ggagaacgag gaaaataagg ag 392

<210> 3
 <211> 475
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(475)
 <223> n = A, T, G, or C

<400> 3
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 ccacgcgtnc gcccacgcgt cccgagagga aaagaaaaaa acctaattta ggagaaagta 120
 aagaagcaat acctgacagc ggaagtctgg aatggagcaa agaaatccca gagcaacgag 180
 aaaacaaaca gcagcagaag aagcgaaaag tccaagataa acagaaatcg gtatcagtca 240
 gcactgtaca ctagagggtt ccatgagatt attgtagact catgatgctg ctatctcaac 300
 cagatgccca ggacaggtgc tctagccatt aggaccacaa atggacatgt cagttattgc 360
 tctgtctaaa caacattccc agtagttgct atattcttca tacaagcata gttaacaaca 420
 aagagccaaa agatcaaaga agggatactt tcagatgggt gtcttgtgtg cttcn 475

<210> 4
 <211> 473
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(473)
 <223> n = A, T, G, or C

<400> 4
 tgggcanann aaanttttga nattcgatcc gcgctgcagg aattcggcac gagacgagga 60
 aaaaaaggaa gggagaggaa aagaaaaaaa cctaataaag gagaaagtaa agaagcaata 120
 cctgacagca aaagtctgga atccagcaga gaaatcccag agcaacgaga aaacaaacag 180

cagcagaaga agcgaaaagt ccaagataaa cagaaatcgg tatcagtcag cactgtacac 240
tagaggggttc catgagatta ttgtagactc atgatgctgc tatctcaacc agatgccag 300
gacaggtgct ctagccatta ggaccacaaa tggacatgct agttattgct ctgtctaaac 360
aacattccca gtagttgcta tattcttcat acaagcatag ttaacaacaa agagccaaaa 420
gatcaaagaa gggatacttt cagatgggtg tcttgtgtgc ttctctgcat ttt 473

<210> 5
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(462)
<223> n = A, T, G, or C

<400> 5
tgggagannn ntttgaaact gagatcgctg canacncnac nangaataaa aggaagggag 60
agggaaagaa aaaaacctaa taaaggagaa agtaaagaat caatttctga cagcaaaagt 120
ctggaatcca tcaaagaaat cccatatcaa cgagaaaaca gacagcagca caaaaagcga 180
aaagtccaag ataaacagaa atcggtatca gtcagcactg tacactagag gggtccatga 240
gattattgta gactcatgat gctgctatct caaccagatg cccaggacag gtgctctatc 300
cattacgacc acaaatggac atgtcagtta ttgctctgtc taaacaacat tcccagtagt 360
tgctatatcc ttcatacaag catagttaac aacaaagagc caaaagatca aagaagggat 420
actttcagat ggttgtcttg tgtgcttctc tgcattttta aa 462

<210> 6
<211> 384
<212> DNA
<213> Homo sapiens

<400> 6
aataatgtgt acaaatgca aagctgactg tgatacctgt ttcaacaaaa atttctgcac 60
aaaatgtaaa agtggatttt acttacacct tggaaagtgc cttgacaatt gccagaagg 120
gttggaagcc aacaaccata ctatggagtg tgtcagtatt gtgcactgtg aggtcagtga 180
atggaatcct tggagtccat gcacgaagaa gggaaaaaca tgtggcttca aaagagggac 240
tgaaacacgg gtccgagaaa taatacagca tccttcagca aagggttaacc tatgtcccc 300
aacaatgag acaagaaagt gtacagtgc aaggaagaag tgcagaagg gagaacgagg 360
aaaaaaagga agggagagga aaag 384

<210> 7
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)..(390)
 <223> n = A, T, G, or C

<400> 7
 cggtgctctg ggatttcttt gctggattcc agacttttgc tgtcaggat tgcttcttta 60
 ctttctcctt tattagggtt ttttcttttc ctctcccttc ctttttttcc tcgttctccc 120
 ttctgacact tcttcctttg cactgtacac tttcttgtct catttggttg gggacatagg 180
 ttaccctttg ctgaaggatg ctgtattatt tctcggaccc gtgtttcagt ccctcttttg 240
 aagccacatg tttttccctt cttcgtgcat ggactccaag gattccattc actgacctca 300
 cagtgcacaa tactgacaca ctccatagta tgggtgttg cttccaaccc ttctgggcaa 360
 ttgtcaaggc actttccaag gtgtaagtan 390

<210> 8
 <211> 1345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (321)..(1235)
 <223> similar to gi4519541 in the genpept database release 114, Run with FASTXY3.3t00, default parameter

<400> 8
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 gccgcccag ttcagtgtt ggataatttg aaagtacaat agttggtttc cctgtccacc 120
 cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgtg 180
 ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat 240
 taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atgcacttgc 300
 gactgatttc ttgggttttt atcattttga actttatgga atacatcggc agccaaaacg 360
 cctcccgggg aaggcgccag cgaagaatgc atcctaacgt tagtcaaggc tgccaaggag 420
 gctgtgcaac atgtcagat tacaatggat gtttgtcatg taagcccaga ctattttttg 480
 ctctggaaag aattggcatg aagcagattg gagtatgtct catcttcatg tccaagtgga 540
 tattatggaa ctcgatatcc agatataaat aatgtgtaca aaatgcaaag ctgactgtga 600
 tacctgtttc aacaaaaatt tctgcacaaa atgtaaaagt ggattttact tacaccttgg 660

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aaagtgcctt gacaattgcc cagaagggtt ggaagccaac aaccatacta tggagtgtgt 720
cagtattgtg cactgtgagg tcagtgaatg gaatccttgg agtccatgca cgaagaaggg 780
aaaaacatgt ggcttcaaaa gagggactga aacacgggtc cgagaaataa tacagcatcc 840
ttcagcaaag ggtaacctat gtcccccaac aaatgagaca agaaagtgtg cagtgcaaag 900
gaagaagtgt cagaaggagg aacgaggaaa aaaaggaagg gagaggaaaa gaaaaaaacc 960
taataaagga gaaagtaaag aagcaatacc tgacagcaaa agtctggaat ccagcaaaga 1020
aatcccagag caacgagaaa acaaacagca gcagaagaag cgaaaagtcc aagataaaca 1080
gaaatcggta tcagtcagca ctgtacacta gagggttcca tgagattatt gtagactcat 1140
gatgctgcta tctcaaccag atgccagga caggtgctct agccattagg accacaaatg 1200
gacatgtcag ttattgctct gtctaaacaa cattcccagt agttgctata ttcttcatac 1260
aagcatagtt aacaacaaag agccaaaaga tcaaagaagg gatactttca gatgggtgtc 1320
ttgtgtgctt ctctgcattt ttaaa 1345

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<210> 9
<211> 1343
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (291)..(1109)

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<400> 9
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cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgtg 180
ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat 240
taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atg cac 296
                                     Met His
                                     1

ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt atg gaa tac 344
Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr
      5                      10                      15

atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat 392
Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His
      20                      25                      30

cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat 440
Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp
      35                      40                      45                      50

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tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt gct ctg gaa	488
Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu	
55 60 65	
aga att ggc atg aag cag att gga gta tgt ctc tct tca tgt cca agt	536
Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser	
70 75 80	
gga tat tat gga act cga tat cca gat ata aat aag tgt aca aaa tgc	584
Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys	
85 90 95	
aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc aca aaa tgt	632
Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys	
100 105 110	
aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac aat tgc cca	680
Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro	
115 120 125 130	
gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc agt att gtg	728
Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val	
135 140 145	
cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc acg aag aag	776
His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys	
150 155 160	
gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg gtc cga gaa	824
Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu	
165 170 175	
ata ata cag cat cct tca gca aag ggt aac cta tgt ccc cca aca aat	872
Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn	
180 185 190	
gag aca aga aag tgt aca gtg caa agg aag aag tgt cag aag gga gaa	920
Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu	
195 200 205 210	
cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct aat aaa gga	968
Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly	
215 220 225	
gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa tcc agc aaa	1016
Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys	
230 235 240	
gaa atc cca gag caa cga gaa aac aaa cag cag cag aag aag cga aaa	1064
Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys	
245 250 255	
gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta cac tag	1109
Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His	
260 265 270	
agggttccat gagattattg tagactcatg atgctgctat ctcaaccaga tgcccaggac	1169
agggtgctcta gccattagga ccacaaatgg acatgtcagt tattgctctg tctaaacaac	1229
attcccagta gttgctatat tcttcataca agcatagtta acaacaaaga gccaaaagat	1289
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<210> 10
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 10

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
 1 5 10 15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
 20 25 30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
 35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
 50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
 65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
 85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
 100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
 115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
 130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
 145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
 165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
 180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
 195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
 210 215 220

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Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
260 265 270

<210> 11
<211> 819

<212> DNA
<213> Homo sapiens

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tgccaaggag gctgtgcaac atgctcagat tacaatggat gtttgtcatg taagcccaga 180
ctattttttg ctctggaaag aattggcatg aagcagattg gagtatgtct ctcttcattg 240
ccaagtggat attatggaac tcgatatcca gatataaata agtgtacaaa atgcaaagct 300
gactgtgata cctgtttcaa caaaaatttc tgcacaaaat gtaaaagtgg attttactta 360
caccttgga agtgccctga caattgcccc gaagggttgg aagccaacaa ccatactatg 420
gagtgtgtca gtattgtgca ctgtgaggtc agtgaatgga atccttggag tccatgcacg 480
aagaagggaa aaacatgtgg cttcaaaaga gggactgaaa cacgggtccg agaaataata 540
cagcatcctt cagcaaaggg taacctatgt cccccaacaa atgagacaag aaagtgtaca 600
gtgcaaagga agaagtgtca gaaggagaaa cgaggaaaaa aaggaaggga gaggaaaaga 660
aaaaaaccta ataaaggaga aagtaaagaa gcaatacctg acagcaaaag tctggaatcc 720
agcaaagaaa tcccagagca acgagaaaac aaacagcagc agaagaagcg aaaagtccaa 780
gataaacaga aatcggtatc agtcagcact gtacactag 819

<210> 12
<211> 822

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (822)

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 Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys
 245 250 255

aag cga aaa gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta 816
 Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val
 260 265 270

cac tag 822
 His

<210> 13
 <211> 273

<212> PRT
 <213> Homo sapiens

<400> 13

Met Gly His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe
 1 5 10 15

Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg
 20 25 30

Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr
 35 40 45

Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe
 50 55 60

Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser
 65 70 75 80

Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys
 85 90 95

Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys
 100 105 110

Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp
 115 120 125

Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val
 130 135 140

Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys
 145 150 155 160

Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg
 165 170 175

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Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro
180 185 190

Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln
195 200 205

Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro
210 215 220

Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu
225 230 235 240

Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys
245 250 255

Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val
260 265 270

His

<210> 14

<211> 160

<212> PRT

<213> Homo sapiens

<400> 14

Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe
1 5 10 15

Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu
20 25 30

Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys
35 40 45

Val Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro
50 55 60

Cys Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr
65 70 75 80

Arg Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys
85 90 95

Pro Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys
100 105 110

Gln Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
115 120 125

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Pro Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu
130 135 140

Glu Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln
145 150 155 160

<210> 15

<211> 21

<212> PRT

<213> Homo sapiens

<400> 15

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15

Glu Tyr Ile Gly Ser

20

<210> 16

<211> 251

<212> PRT

<213> Homo sapiens

<400> 16

Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val
1 5 10 15

Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly
20 25 30

Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly
35 40 45

Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr
50 55 60

Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp
65 70 75 80

Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
85 90 95

Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu
100 105 110

Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu
115 120 125

Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr
130 135 140

Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu Ile Ile Gln
145 150 155 160

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His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg
165 170 175

Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys
180 185 190

Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys
195 200 205

Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro
210 215 220

Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys Val Gln Asp
225 230 235 240

Lys Gln Lys Ser Val Ser Val Ser Thr Val His
245 250

<210> 17

<211> 23

<212> PRT

<213> Homo sapiens

<400> 17

Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys
1 5 10 15

Ser Gly Phe Tyr Leu His Leu
20

<210> 18

<211> 46

<212> PRT

<213> Homo sapiens

<400> 18

Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn
1 5 10 15

Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly
20 25 30

Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn
35 40 45

<210> 19

<211> 20

<212> PRT

<213> Homo sapiens

<400> 19

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<400> 23

Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
1 5 10

<210> 24

<211> 20

<212> PRT

<213> Homo sapiens

<400> 24

Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly
1 5 10 15

Lys Thr Cys Gly
20

<210> 25

<211> 229

<212> PRT

<213> Mus musculus

<400> 25

Val Gly Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile Ser Ala
1 5 10 15

Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser Glu Val
20 25 30

Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu Glu Arg
35 40 45

Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro Pro Gly
50 55 60

Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys Cys Lys
65 70 75 80

Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr Lys Cys
85 90 95

Gln Glu Ala Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala Cys Pro
100 105 110

Glu Gly Ser Thr Ala Ala Asn Ser Thr Met Glu Cys Gly Ser Pro Ala
115 120 125

Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser Lys Lys
130 135 140

Arg Lys Leu Cys Gly Phe Arg Lys Gly Ser Glu Glu Arg Thr Arg Arg
145 150 155 160

Val Leu His Ala Pro Gly Gly Asp His Thr Thr Cys Ser Asp Thr Lys
165 170 175

00004912 062301

Glu Thr Arg Lys Cys Thr Val Arg Arg Thr Pro Cys Pro Glu Gly Gln
180 185 190
Lys Arg Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn Ala Asn Arg His
195 200 205
Pro Ala Arg Lys Asn Ser Lys Glu Pro Arg Ser Asn Ser Arg Arg His
210 215 220
Lys Gly Gln Gln Gln
225

<210> 26
<211> 265
<212> PRT
<213> Homo sapiens

<400> 26

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15
Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20 25 30
Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45
Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60
Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80
Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95
Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110
Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220

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ggagcgggtc ctgctcagaa cgccagaagc agctcgggtc tctccagcgc cccttgacca 60
tggtgcggt acccacggcg tccgcttccc tgcgctcccg gggtcctgc cacagccgca 120
gccgctgcag cctctgagcc ccaggggcca ctgctcgctt ggattccgcc cgcagccgcc 180
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gagaaaaaag ggaaacatta caggggttact atg cac ttg cga ctg att tct tgt 534
                               1             5
                               Met His Leu Arg Leu Ile Ser Cys

ttt ttt atc att ttg aac ttt atg gaa tac att ggc agc caa aac gcc 582
Phe Phe Ile Ile Leu Asn Phe Met Glu Tyr Ile Gly Ser Gln Asn Ala
      10              15              20

tcc cga gga agg cgc cag cga aga atg cat cct aat gtc agt caa ggc 630
Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val Ser Gln Gly
      25              30              35              40

tgc caa gga ggc tgt gca acg tgt tca gat tac aat ggc tgt ttg tca 678
Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly Cys Leu Ser
              45              50              55

tgt aag ccc aga ctg ttt ttt gtt ctg gaa agg att ggc atg aag cag 726
Cys Lys Pro Arg Leu Phe Phe Val Leu Glu Arg Ile Gly Met Lys Gln
              60              65              70

ata gga gtg tgt ctc tct tcg tgt cca agt gga tat tac gga act cga 774
Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr Gly Thr Arg
      75              80              85

tat cca gat ata aat aaa tgt aca aaa tgc aaa gtt gac tgt gat acc 822
Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Val Asp Cys Asp Thr
      90              95              100

tgt ttc aac aaa aat ttc tgc aca aag tgt aaa agt gga ttt tac tta 870
Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu
     105              110              115              120

cac ctt gga aag tgc ctt gac agt tgc cca gaa ggg tta gaa gcc aac 918
His Leu Gly Lys Cys Leu Asp Ser Cys Pro Glu Gly Leu Glu Ala Asn
              125              130              135

aat cat act atg gaa tgt gtc agt att gta cac tgt gag gcc agt gaa 966
Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu Ala Ser Glu
              140              145              150

tgg agt cca tgg agt cca tgt atg aag aaa gga aaa aca tgt ggc ttc 1014
Trp Ser Pro Trp Ser Pro Cys Met Lys Lys Gly Lys Thr Cys Gly Phe
              155              160              165

aaa agg ggg act gaa aca cgg gtc cga gat ata cta cag cat cct tca 1062
Lys Arg Gly Thr Glu Thr Arg Val Arg Asp Ile Leu Gln His Pro Ser
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gcc aag ggt aag ggt aac ctg tgc ccc cca acc agc gag aca aga act 1110
Ala Lys Gly Lys Gly Asn Leu Cys Pro Pro Thr Ser Glu Thr Arg Thr
185 190 195 200

tgt ata gta caa aga aag aag tgt tca aag gga gag cga gga aaa aag 1158
Cys Ile Val Gln Arg Lys Lys Cys Ser Lys Gly Glu Arg Gly Lys Lys
205 210 215

gga aga gag aga aaa cga aaa aaa ctg aat aaa gaa gaa aga aag gaa 1206
Gly Arg Glu Arg Lys Arg Lys Lys Leu Asn Lys Glu Glu Arg Lys Glu
220 225 230

aca agc tcc tcc tct gac agc aaa ggt ttg gag tcc agc att gag acc 1254
Thr Ser Ser Ser Ser Asp Ser Lys Gly Leu Glu Ser Ser Ile Glu Thr
235 240 245

cca gac cag cag gaa aac aaa gag agg cag cag cag cag aag aga aga 1302
Pro Asp Gln Gln Glu Asn Lys Glu Arg Gln Gln Gln Gln Lys Arg Arg
250 255 260

gcc cga gac aag caa cag aaa tcg gta tca gtc agc act gta cac 1347
Ala Arg Asp Lys Gln Gln Lys Ser Val Ser Val Ser Thr Val His
265 270 275

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<211> 279
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 <213> Mus musculus

<400> 32

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Met His Leu Arg Leu Ile Ser Cys Phe Phe Ile Ile Leu Asn Phe Met
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Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
      20           25           30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
      35           40           45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Val
      50           55           60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
      65           70           75           80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
      85           90           95

Lys Cys Lys Val Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
      100          105          110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Ser
      115          120          125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
      130          135          140

Ile Val His Cys Glu Ala Ser Glu Trp Ser Pro Trp Ser Pro Cys Met
      145          150          155          160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
      165          170          175

Arg Asp Ile Leu Gln His Pro Ser Ala Lys Gly Lys Gly Asn Leu Cys
      180          185          190

Pro Pro Thr Ser Glu Thr Arg Thr Cys Ile Val Gln Arg Lys Lys Cys
      195          200          205

Ser Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
      210          215          220

Leu Asn Lys Glu Glu Arg Lys Glu Thr Ser Ser Ser Ser Asp Ser Lys
      225          230          235          240

Gly Leu Glu Ser Ser Ile Glu Thr Pro Asp Gln Gln Glu Asn Lys Glu
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Arg Gln Gln Gln Gln Lys Arg Arg Ala Arg Asp Lys Gln Gln Lys Ser
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Val Ser Val Ser Thr Val His
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<210> 33
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21

<213> Homo sapiens

<400> 34

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Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45
Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60
Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80
Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95
Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110
Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220
Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240
Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255
Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
260 265 270

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<210> 41
<211> 30
<212> DNA
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<400> 41
tggtggcttt ctcccctact agatatacct 30

<210> 42
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 42
gatttttaggt gacactatag 20

<210> 43
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 43
ccgctcgagc caccatgcac ttgcgactga tttc 34

<210> 44
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 44
attgaattcc tagtgtacag tgctgactg 29

<210> 45
<211> 84
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

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<222> (1)..(81)

<400> 45,

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tgcaggagga ggtatctctg agtgtgcagc acagaatcgc atgaccacc ttaaccttcc 1200
tgttgatcatg gaaggatgca cggctgctct gtccactgtg attcctagcc ctctcaagat 1260
cactgctttc tgaagaattt gcaatgactc tggcttctgg ctgcttatct ctggacaccc 1320
gttctccacc agttgtacag ttcattgtaat ctacttggct taattgattt tccacttctc 1380
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<210> 48
<211> 292
<212> PRT
<213> Homo sapiens

<400> 48
Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
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Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20 25 30
Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45
Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60
Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80
Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95
Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110
Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220

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See
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cont

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala
260 265 270

Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg
275 280 285

Arg Arg Tyr Leu
290

full
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cont

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